

# SEQUENCE LISTING

<110> Kazuko, SHINOZAKI  
Mie, KASUGA

<120> Environmental Stress-Tolerant Plants

<130> 382.1029DIV1

<150> JP292348/1998  
US 09/301,217

<151> 1998-10-14  
1999-04-28

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<170> PatentIn Ver. 2.0

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Tyr																	
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Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly
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Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp
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Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile
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Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys
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Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
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Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Ile Ala
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Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile Gln Lys Ala Ala
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Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys His Met Thr Thr
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ag atg gct gta tat gaa caa acc gga acc gag cag ccg aag aaa agg 227
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65	70	75	
gga gtt aga caa agg att tgg ggt aaa tgg gtt gca gag att cga gaa			467
Gly Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu			
80	85	90	95
ccg aaa ata gga act aga ctt tgg ctt ggt act ttt cct acc gcg gaa			515
Pro Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu			
100	105	110	
aaa gct gct tcc gct tat gat gaa gcg gct acc gct atg tac ggt tca			563
Lys Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser			
115	120	125	
ttg gct cgt ctt aac ttc cct cag tct gtt ggg tct gag ttt act agt			611
Leu Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser			
130	135	140	
acg tct agt caa tct gag gtg tgt acg gtt gaa aat aag gcg gtt gtt			659
Thr Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val			
145	150	155	
tgt ggt gat gtt tgt gtg aag cat gaa gat act gat tgt gaa tct aat			707
Cys Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn			
160	165	170	175
cca ttt agt cag att tta gat gtt aga gaa gag tct tgt gga acc agg			755
Pro Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg			
180	185	190	
ccg gac agt tgc acg gtt gga cat caa gat atg aat tct tcg ctg aat			803
Pro Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn			
195	200	205	
tac gat ttg ctg tta gag ttt gag cag cag tat tgg ggc caa gtt ttg			851
Tyr Asp Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu			
210	215	220	
cag gag aaa gag aaa ccg aag cag gaa gaa gag gag ata cag caa cag			899
Gln Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Glu Ile Gln Gln Gln			
225	230	235	
caa cag gaa cag caa cag caa cag ctg caa ccg gat ttg ctt act gtt			947
Gln Gln Glu Gln Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val			
240	245	250	255
gca gat tac ggt tgg cct tgg tct aat gat att gta aat gat cag act			995
Ala Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr			
260	265	270	
tct tgg gat cct aat gag tgc ttt gat att aat gaa ctc ctt gga gat			1043
Ser Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp			
275	280	285	
ttg aat gaa cct ggt ccc cat cag agc caa gac caa aac cac gta aat			1091
Leu Asn Glu Pro Gly Pro His Gln Ser Gln Asp Gln Asn His Val Asn			
290	295	300	
tct ggt agt tat gat ttg cat ccg ctt cat ctc gag cca cac gat ggt			1139
Ser Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly			
305	310	315	
cac gag ttc aat ggt ttg agt tct ctg gat att tgagagttct gaggcaatgg			1192
His Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile			
320	325	330	
tcctacaaga ctacaacata atctttggat tgatcatagg agaaacaaga aataggtggt			1252
aatgatctga ttcacaatga aaaaatattt aataactcta tagtttttgt tctttccttg			1312
gatcatgaac tgttgcttct catctattga gttaatatag cgaatagcag agtttctctc			1372

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tttcttctct ttgtagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaayh sakmabgcar 1432
srcsdvsnaa nntnatnar sarchcntrr agrctrascn csrscaswash tskbabarak 1492
aantamaysa kmasrngnga c 1513

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<210> 10
<211> 330
<212> PRT
<213> Arabidopsis thaliana

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<400> 10
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Ser Arg Ala Arg Ala Gly Gly Leu Thr Val Ala Asp Arg Leu Lys Lys
 20          25          30
Trp Lys Glu Tyr Asn Glu Ile Val Glu Ala Ser Ala Val Lys Glu Gly
 35          40          45
Glu Lys Pro Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys
 50          55          60
Met Lys Gly Lys Gly Gly Pro Asp Asn Ser His Cys Ser Phe Arg Gly
 65          70          75          80
Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro
 85          90          95
Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu Lys
100          105          110
Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser Leu
115          120          125
Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser Thr
130          135          140
Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val Cys
145          150          155          160
Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn Pro
165          170          175
Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg Pro
180          185          190
Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn Tyr
195          200          205
Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu Gln
210          215          220
Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Glu Ile Gln Gln Gln Gln
225          230          235          240
Gln Glu Gln Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val Ala
245          250          255
Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr Ser
260          265          270
Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp Leu
275          280          285
Asn Glu Pro Gly Pro His Gln Ser Gln Asp Gln Asn His Val Asn Ser
290          295          300
Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly His
305          310          315          320
Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile
325          330

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<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

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<220>  
 <223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 11  
 aagcttaagc ttacatcagt ttgaaagaaa 30

<210> 12  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 12  
 aagcttaagc ttgctttttg gaactcatgt c 31

<210> 13  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide based on DREB1A gene and having BamHI site.

<400> 13  
 aagcttaagc ttgccataga tgcaattcaa tc 32

<210> 14  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide based on DREB1A gene and having BamHI site.

<400> 14  
 aagcttaagc ttttccaaag atttttttct ttccaa 36

<210> 15  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 15  
 ggatccgat ccatgaactc attttctgct 30

<210> 16

<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 16  
ggatccggat ccttaataac tccataacga ta 32

<210> 17  
<211> 941  
<212> DNA  
<213> Arabidopsis thaliana  
<400> 17

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cttatataca ttatatgtta attttttgta acaaaatggt tttattatta ttatagaatt 180
ttactgggta aattaaaaat gaatagaaaa ggtgaattaa gaggagagag gaggtaaaca 240
ttttcttcta ttttttcata ttttcaggat aaattattgt aaaagtttac aagatttcca 300
tttgactagt gtaaatgagg aatattctct agtaagatca ttatttcata tacttctttt 360
atcttctacc agtagaggaa taaacaatat ttagctcctt tgtaaataca aattaatttt 420
ccttcttgac atcattcaat ttttaattta cgtataaaat aaaagatcat acctattaga 480
acgattaagg agaaatacaa ttcgaatgag aaggatgtgc cgtttggtat aataaacagc 540
cacacgacgt aaacgtaaaa tgaccacatg atgggccaat agacatggac cgactactaa 600
taatagtaag ttacatttta ggatggaata aatatcatal cgacatcagt tttgaaagaa 660
aagggaataa aagaaaaaat aaataaaaaga tatactaccg acatgagttc caaaaagcaa 720
aaaaaaaagat caagccgaca cagacacgcg tagagagcaa aatgactttg acgtcacacc 780
acgaaaacag acgcttcata cgtgtccctt tatctctctc agtctctcta taaacttagt 840
gagaccctcc tctgttttac tcacaaatat gcaaaactaga aaacaatcat caggaataaa 900
gggtttgatt acttctattg gaaagaaaaa aatctttgga a 941
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<210> 18  
<211> 71  
<212> DNA  
<213> Arabidopsis thaliana

<400> 18  
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta ccgacatgag 60  
ttccaaaaag c 71

<210> 19  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 19  
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatattt tcgacatgag 60  
ttccaaaaag c 71

<210> 20  
<211> 71

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 20  
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta cttttatgag 60  
ttccaaaaag c 71

<210> 21  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 21  
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta ccgacaaaag 60  
ttccaaaaag c 71

<210> 22  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence outside the DRE region.

<400> 22  
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caacaaaaag c 71

<210> 23  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence outside the DRE region.

<400> 23  
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta ccgacatgag 60  
ttcggttaag c 71